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SEQUENCE LISTING

15 (1) GENERAL INFORMATION:

(i) APPLICANT: Drazen MD, Jeffrey

(ii) TITLE OF INVENTION: Diagnosing Asthma Patients Predisposed to  
Adverse Beta-Agonist Reactions

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Choate, Hall & Stewart

(B) STREET: 53 State Street

(C) CITY: Boston

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jarrell PhD, Brenda H.

(B) REGISTRATION NUMBER: 39,223

(C) REFERENCE/DOCKET NUMBER: 0092662-0010

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617 248 4000

(B) TELEFAX: 617 248 5000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Human Beta-2-Adrenergic Receptor Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg  
1 5 10 15  
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp  
20 25 30  
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val  
35 40 45  
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu  
50 55 60  
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu  
65 70 75 80  
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met  
85 90 95  
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile  
100 105 110  
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala  
115 120 125  
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu  
130 135 140  
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val  
145 150 155 160  
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala  
165 170 175  
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp  
180 185 190  
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe

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Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln  
210 215 220

Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe  
225 230 235 240

His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His  
245 250 255

Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu  
260 265 270

Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro  
275 280 285

Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg  
290 295 300

Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly  
305 310 315 320

Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe  
325 330 335

Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn  
340 345 350

Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val  
355 360 365

Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr  
370 375 380

Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp  
385 390 395 400

Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu  
405 410

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN Beta-2-Adrenergic Receptor Gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5  
CCCCGGTTCA AGAGATTCTC CTGTCTCAGC CTCCCGAGTA GCTGGGACTA CAGGTACGTG 60  
CCACCACACC TGGCTAATTT TTGTATTTTT AGTAGAGACA AGAGTTACAC CATATTGGCC 120  
10 AGGATCTTTT GCTTCTATA GCTTCAAAAT GTTCTTAATG TTAAGACATT CTTAATACTC 180  
TGAACCATAT GAATTTGCCA TTTTGGTAAG TCACAGACGC CAGATGGTGG CAATTTCACA 240  
TGGCACAACC CGAAAGATTA ACAAACATATC CAGCAGATGA AAGGATTTTT TTTAGTTTCA 300  
15 TTGGGTTTAC TGAAGAAATT GTTTGAATTC TCATTGCATC TCCAGTTCAA CAGATAATGA 360  
GTGAGTGATG CCACACTCTC AAGAGTTAAA AACAAAACAA CAAAAAATT AAAACAAAAG 420  
20 CACACAACCTT TCTCTCTCTG TCCCAAATA CATACTTGCA TACCCCGCT CCAGATAAAA 480  
TCCAAAGGGT AAAACTGTCT TCATGCCTGC AAATTCCTAA GGAGGGCACC TAAAGTACTT 540  
GACAGCGAGT GTGCTGAGGA AATCGGCAGC TGTGAAGTC ACCTCCTGTG CTCTTGCCAA 600  
25 ATGTTTGAAA GGGAATACAC TGGGTTACCG GGTGTATGTT GGGAGGGGAG CATTATCAGT 660  
GCTCGGGTGA GGCAAGTTCG GAGTACCCAG ATGGAGACAT CCGTGTCTGT GTCGCTCTGG 720  
ATGCCTCCAA GCCAGCGTGT GTTACTTTC TGTGTGTGTC ACCATGTCTT TGTGCTTCTG 780  
30 GGTGCTTCTG TGTTTGTTTC TGGCCGCGTT TCTGTGTTGG ACAGGGGTGA CTTTGTGCCG 840  
GATGGCTTCT GTGTGAGAGC GCGCGCGAGT GTGCATGTCG GTGAGCTGGG AGGGTGTGTC 900  
35 TCAGTGTCTA TGGCTGTGGT TCGGTATAAG TCTGAGCATG TCTGCCAGGG TGTATTTGTG 960  
CCTGTATGTG CGTGCCTCGG TGGGCACTCT CGTTTCCTTC CGAATGTGGG GCAGTGCCGG 1020  
TGTGCTGCCC TCTGCCTTGA GACCTCAAGC CGCGCAGGCG CCCAGGGCAG GCAGGTAGCG 1080  
40 GCCACAGAAG AGCCAAAAGC TCCCGGGTTG GCTGGTAAGG ACACCACCTC CAGCTTTAGC 1140  
CCTCTGGGGC CAGCCAGGGT AGCCGGGAAG CAGTGGTGGC CCGCCCTCCA GGGAGCAGTT 1200  
45 GGGCCCCGCC CGGGCCAGCC CCAGGAGAAG GAGGGCGAGG GGAGGGGAGG GAAAGGGGAG 1260  
GAGTGCCTCG CCCCTTCGCG GCTGCCGGCG TGCCATTGGC CGAAAGTTCC CGTACGTCAC 1320  
GGCGAGGGCA GTTCCCCTAA AGTCCTGTGC ACATAACGGG CAGAACGCAC TGCGAAGCGG 1380  
50 CTTCTTCAGA GCACGGGCTG GAACTGGCAG GCACCGCGAG CCCCTAGCAC CCGACAAGCT 1440  
GAGTGTGCAG GACGAGTCCC CACCACACCC ACACCACAGC CGCTGAATGA GGCTTCCAGG 1500

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	CGTCCGCTCG	CGGCCCCGAG	AGCCCCGCCG	TGGGTCCGCC	CGCTGAGGCG	CCCCAGCCA	1560
	GTGCGCTTAC	CTGCCAGACT	GCGCGCCATG	GGGCAACCCG	GGAACGGCAG	CGCCTTCTTG	1620
5	CTGGCACCCA	ATAGAAGCCA	TGCGCCGGAC	CACGACGTCA	CGCAGCAAAG	GGACGAGGTG	1680
	TGGGTGGTGG	GCATGGGCAT	CGTCATGTCT	CTCATCGTCC	TGGCCATCGT	GTTTGGCAAT	1740
	GTGCTGGTCA	TCACAGCCAT	TGCCAAGTTC	GAGCGTCTGC	AGACGGTCAC	CAACTACTTC	1800
10	ATCACTTCAC	TGGCCTGTGC	TGATCTGGTC	ATGGGCCTGG	CAGTGGTGCC	CTTTGGGGCC	1860
	GCCCATATTC	TTATGAAAAT	GTGGACTTTT	GGCAACTTCT	GGTGCGAGTT	TTGGACTTCC	1920
15	ATTGATGTGC	TGTGCGTCAC	GGCCAGCATT	GAGACCCTGT	GCGTGATCGC	AGTGGATCGC	1980
	TACTTTGCCA	TTACTTCACC	TTTCAAGTAC	CAGAGCCTGC	TGACCAAGAA	TAAGGCCCGG	2040
	GTGATCATTC	TGATGGTGTG	GATTGTGTCA	GGCCTTACCT	CCTTCTTGCC	CATTTCAGATG	2100
20	CACTGGTACC	GGGCCACCCA	CCAGGAAGCC	ATCAACTGCT	ATGCCAATGA	GACCTGCTGT	2160
	GACTTCTTCA	CGAACCAAGC	CTATGCCATT	GCCTCTTCCA	TCGTGTCCTT	CTACGTTCCC	2220
25	CTGGTGATCA	TGGTCTTCGT	CTACTCCAGG	GTCTTTCAGG	AGGCCAAAAG	GCAGCTCCAG	2280
	AAGATTGACA	AATCTGAGGG	CCGCTTCCAT	GTCCAGAACC	TTAGCCAGGT	GGAGCAGGAT	2340
	GGGCGGACGG	GGCATGGACT	CCGCAGATCT	TCCAAGTTCT	GCTTGAAGGA	GCACAAAGCC	2400
30	CTCAAGACGT	TAGGCATCAT	CATGGGCACT	TTCACCCTCT	GCTGGCTGCC	CTTCTTCATC	2460
	GTTAACATTG	TGCATGTGAT	CCAGGATAAC	CTCATCCGTA	AGGAAGTTTA	CATCCTCCTA	2520
35	AATTGGATAG	GCTATGTCAA	TTCTGGTTTC	AATCCCCTTA	TCTACTGCCG	GAGCCCAGAT	2580
	TTCAGGATTG	CCTTCCAGGA	GCTTCTGTGC	CTGCGCAGGT	CTTCTTTGAA	GGCCTATGGG	2640
	AATGGCTACT	CCAGCAACGG	CAACACAGGG	GAGCAGAGTG	GATATCACGT	GGAACAGGAG	2700
40	AAAGAAAATA	AACTGCTGTG	TGAAGACCTC	CCAGGCACGG	AAGACTTTGT	GGGCCATCAA	2760
	GGTACTGTGC	CTAGCGATAA	CATTGATTCA	CAAGGGAGGA	ATTGTAGTAC	AAATGACTCA	2820
45	CTGCTGTAAA	GCAGTTTTTC	TACTTTTAAA	GACCCCCCCC	CCCCAACAG	AACACTAAAC	2880
	AGACTATTTA	ACTTGAGGGT	AATAAACTTA	GAATAAAATT	GTAAAAATTG	TATAGAGATA	2940
	TGCAGAAGGA	AGGGCATCCT	TCTGCCTTTT	TTATTTTTTT	AAGCTGTAAA	AAGAGAGAAA	3000
50	ACTTATTTGA	GTGATTATTT	GTTATTTGTA	CAGTTCAGTT	CCTCTTTGCA	TGGAATTTGT	3060
	AAGTTTATGT	CTAAAGAGCT	TTAGTCCTAG	AGGACCTGAG	TCTGCTATAT	TTTCATGACT	3120

TTTCCATGTA TCTACCTCAC TATTCAAGTA TTAGGGGTAA TATATTGCTG CTGGTAATTT 3180  
 GTATCTGAAG GAGATTTTCC TTCCTACACC CTTGGACTTG AGGATTTTGA GTATCTCGGA 3240  
 5 CCTTTCAGCT GTGAACATGG ACTCTTCCCC CACTCCTCTT ATTTGCTCAC ACGGGGTATT 3300  
 TTAGGCAGGG ATTTGAGGAG CAGCTTCAGT TGTTTTCCCG AGCAAAGGTC TAAAGTTTAC 3360  
 AGTAAATAAA ATGTTTGACC ATGCCTTCAT TGCACCTGTT TGTCCAAAAC CCCTTGACTG 3420  
 10 GAGTGCTGTT GCCTCCCCCA CTGGAAACCG C 3451

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: wild-type forward primer A1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCTCTTGCT GGCACCCAAA A 21

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: polymorphism-specific primer A2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCTTCTTGC TGGCACCCAA AG

22

5 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vii) IMMEDIATE SOURCE:

(B) CLONE: reverse primer Rev

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATAACCT CATCCGTAAG G

21

25 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vii) IMMEDIATE SOURCE:

(B) CLONE: wild-type forward primer B1

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGACCACG ACGTCACGCA AC

22

45 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

5 (B) CLONE: polymorphism-specific forward primer B2 (xi) SEQUENCE  
DESCRIPTION: SEQ ID NO:7:

CCGGACCACG ACGTCACGCA AG

22

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: Beta-golbin forward primer BG1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTGTCATCA CTTAGACCTC

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: Beta-globin reverse primer BG2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGACGAATG ATTGCATCAG

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